

1636
TECH CENTER 1600/2900

NOV 14 2001

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#14
600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995D

DATE: 10/29/2001

TIME: 14:44:35

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\10292001\I236995D.raw

4 <110> APPLICANT: Mahajan, Pramod
 5 Zuo, Zhuang
 7 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and its
 8 Uses
 10 <130> FILE REFERENCE: 5718-34
 12 <140> CURRENT APPLICATION NUMBER: US 09/236,995D
 13 <141> CURRENT FILING DATE: 1999-01-26
 15 <150> PRIOR APPLICATION NUMBER: US 60/072,785
 16 <151> PRIOR FILING DATE: 1998-01-27
 18 <160> NUMBER OF SEQ ID NOS: 5
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2949
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Zea mays
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)...(2949)
 31 <221> NAME/KEY: misc feature
 32 <222> LOCATION: 1584, 1588, 2078, 2107
 33 <223> OTHER INFORMATION: n = A,T,C or G
 35 <400> SEQUENCE: 1
 36 atg gcg gcg ccg cca aag gcg tgg aag gcg gag tat gcc aag tct ggg 48
 37 Met Ala Ala Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
 38 1 5 10 15
 40 cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
 41 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
 42 20 25 30
 44 cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
 45 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 46 35 40 45
 48 atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
 49 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 50 50 55 60
 52 tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
 53 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 54 65 70 75 80
 56 gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288
 57 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 58 85 90 95
 60 aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336
 61 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 62 100 105 110
 64 cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc 384
 65 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 66 115 120 125
 68 cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432

ENTERED

P.5

DNA Sequence; it is not necessary
 that unknown PRTs in coded
 regions are listed. nuf

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69 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
70      130      135      140
72 tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag 480
73 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
74 145      150      155      160
76 aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg 528
77 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
78      165      170      175
80 ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt 576
81 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
82      180      185      190
84 tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc 624
85 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
86      195      200      205
88 agg tta gat gaa agt aca tct gaa ggt aca gtg cga aac aaa ggg caa 672
89 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
90      210      215      220
92 ctt gta gac cca cgt ggt tcc aat act agt tca gct gat atc caa cta 720
93 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
94 225      230      235      240
96 aag ctt aag gag caa agt gac aca ctt tgg aag tta aag gat gga ctt 768
97 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
98      245      250      255
100 aag act cat gta tcg gct gct gaa tta agg gat atg ctt gag gct aat 816
101 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
102      260      265      270
104 ggg cag gat aca tca gga cca gaa agg cac cta ttg gat cgc tgt gcg 864
105 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
106      275      280      285
108 gat gga atg cta ttt gga gcg ctg ggt cct tgc cca gtc tgt gct aat 912
109 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
110      290      295      300
112 ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtg tca 960
113 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
114 305      310      315      320
116 gag tgg tcc aag tgt aca tac tct gcc aca gaa cct gtc cgc gtt aag 1008
117 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
118      325      330      335
120 aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag 1056
121 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
122      340      345      350
124 tgg ttc aaa tct caa aag gtt aag aaa cca gag agg gtt ctt cca cca 1104
125 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
126      355      360      365
128 atg tca cct gag aaa tct gga agt aaa gca act cag aga aca tca ttg 1152
129 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
130      370      375      380
132 ctg tct tct aaa ggg ttg gat aaa tta agg ttt tct gtt gta gga caa 1200
133 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln

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```

134 385          390          395          400
136 tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt 1248
137 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
138          405          410          415
140 gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca 1296
141 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
142          420          425          430
144 tgt ggt gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg 1344
145 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
146          435          440          445
148 ctg aag ata cca att gta agg gag ggt tac att gga gaa tgt gtt aaa 1392
149 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
150          450          455          460
152 aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag 1440
153 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
154 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575
156 tcc tca aaa ggc mgt act gtc act gtt aaa gtt aag ggc cga agt get 1488
W--> 157 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
158          485          490          495          500          505          510          515          520          525          530          535          540          545          550          555          560          565          570          575
160 tgt tca tya agt cct cyg gtt tgc aag aat act gct cac att cct tra 1536
W--> 161 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
162          500          505          510          515          520          525          530          535          540          545          550          555          560          565          570          575
W--> 164 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn 1584
W--> 165 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
166          515          520          525          530          535          540          545          550          555          560          565          570          575
W--> 168 cac mag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat 1632
W--> 169 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
170          530          535          540          545          550          555          560          565          570          575
172 gat ggg tct gag tgc tac gta ttt cgt aag tgg gga cgg gtt ggg agt 1680
173 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
174 545          550          555          560          565          570          575
176 gag aaa att gga ggg caa aaa ctg gag gag atg tca aaa act gag gca 1728
177 Glu Lys Ile Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
178          565          570          575
180 atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg 1776
181 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
182          580          585          590
184 gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct ggg aga ttt 1824
185 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
186          595          600          605
188 tac cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aaa 1872
189 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
190          610          615          620
192 gat atc agt gaa atg aaa agt tct ctt gct cct caa ttg cta gaa ctc 1920
193 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
194 625          630          635          640
196 atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa 1968
197 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
198          645          650          655

```

These Xaas
are not boxed
as individual
locus nor as
range for
sequence listing

OR.
DNA

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\10292001\I236995D.raw

200 ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra 2016
 W--> 201 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa not listed
 202 660 665 670
 204 aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt 2064
 W--> 205 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
 206 675 680 685 2107
 W--> 208 gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg 2112
 W--> 209 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
 210 690 695 700 not listed
 212 ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc 2160
 W--> 213 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
 214 705 710 715 720
 216 ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt 2208
 217 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
 218 725 730 735
 220 gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat 2256
 221 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
 222 740 745 750
 224 agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt 2304
 225 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
 226 755 760 765
 228 gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag 2352
 229 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
 230 770 775 780
 232 cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg 2400
 233 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
 234 785 790 795 800
 236 gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag 2448
 237 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
 238 805 810 815
 240 tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac 2496
 241 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
 242 820 825 830
 244 ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga 2544
 245 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
 246 835 840 845
 248 att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc 2592
 249 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
 250 850 855 860
 252 ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg 2640
 253 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
 254 865 870 875 880
 256 gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta 2688
 257 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
 258 885 890 895
 260 gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca 2736
 261 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
 262 900 905 910
 264 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784

RAW SEQUENCE LISTING

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Input Set : A:\Seqlist.txt

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265 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
266          915          920          925
268 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
269 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
270          930          935          940
272 ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
273 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
274 945          950          955          960
276 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
277 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
278          965          970          975
280 cgt ttc cat cac aag agg tag 2949
281 Arg Phe His His Lys Arg *
282          980
285 <210> SEQ ID NO: 2
286 <211> LENGTH: 982
287 <212> TYPE: PRT
288 <213> ORGANISM: Zea mays
290 <220> FEATURE:
291 <221> NAME/KEY: VARIANT
292 <222> LOCATION: 485, 499, 502, 512, 513, 521, 528, 530, 659, 671, 672, 676,
293      683, 684, 685, 686, 693, 699, 703, 706, 707, 708, 709, 710
294 <223> OTHER INFORMATION: Xaa = Any Amino Acid
296 <400> SEQUENCE: 2
297 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
298 1          5          10          15
299 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
300          20          25          30
301 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
302          35          40          45
303 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
304          50          55          60
305 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
306 65          70          75          80
307 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
308          85          90          95
309 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
310          100          105          110
311 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
312          115          120          125
313 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
314          130          135          140
315 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
316 145          150          155          160
317 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
318          165          170          175
319 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
320          180          185          190
321 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala

```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <223> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/236,995D

DATE: 10/29/2001

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Input Set : A:\Seqlist.txt

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L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2